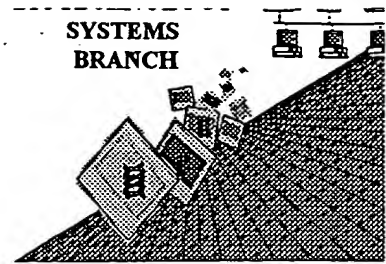


RAW SEQUENCE LISTING **ERROR REPORT**



#8

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/445,375

Art Unit / Team No. : 1632

Date Processed by STIC: 5/18/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/445,375

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 **Variable Length** Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 **Skipped Sequences (OLD RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 **Skipped Sequences (NEW RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 **Use of <213>Organism (NEW RULES)** Sequence(s) are missing this mandatory field or its response.
- 12 **Use of <220>Feature (NEW RULES)** Sequence(s) are missing the <220>Feature and associated headings
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

1632

RAW SEQUENCE LISTING DATE: 05/18/2000
 PATENT APPLICATION: US/09/445,375 TIME: 12:23:30

Input Set : A:\DU23SEQ.txt
 Output Set: N:\CRF3\05182000\I445375.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Kingsman, Susan M
 4 Bebbington, C.
 5 Ellard, F.
 6 Carroll, Miles
 8 <120> TITLE OF INVENTION: VECTOR
 10 <130> FILE REFERENCE: DY0U23.001APC
 12 <140> CURRENT APPLICATION NUMBER: US/09/445,375
 13 <141> CURRENT FILING DATE: 1999-12-02
 15 <160> NUMBER OF SEQ ID NOS: 24
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give source of genetic material -
 see circled portion
 of item 12
 on Eva summary
 sheet

see
 item 10
 on Eva
 summary
 sheet

item 10
 on Eva
 summary
 sheet

RAW SEQUENCE LISTING DATE: 05/18/2000
 PATENT APPLICATION: US/09/445,375 TIME: 12:23:30

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item 10 for all labeled lines

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item 10

RAW SEQUENCE LISTING DATE: 05/18/2000
 PATENT APPLICATION: US/09/445,375 TIME: 12:23:30

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/445,375
 DATE: 05/18/2000
 TIME: 12:23:30

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/445,375
 DATE: 05/18/2000
 TIME: 12:23:30

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234 cggggagcgg ggacaagcgc accctgcctt gcctgatcca gaacttcacg cctgaggaca 1860
235 tctcgggtga gtggctgcac aacgaggtgc agtcccgga cgcccggcac agcacgacgc 1920
236 agcccgcaa gaccaaaggg tccggcttct tctcttcag ccgctggag gtgaccaggg 1980
237 ccgaatggga gcagaagat gatctcatct gccgtgcagt ccatgaggca gcgagcccct 2040
238 cacagaccgt ccagcgagcg gtgtctgtaa atcccggtaa atgagagctc 2090

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240 <210> SEQ ID NO: 7
241 <211> LENGTH: 945
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence DNA
248 <400> SEQUENCE: 7

```

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249 atggcttgca attgtcagtt gatgcaggat acaccactcc tcaagtttcc atgtccaagg 60
250 ctcattcttc tctttgtgct gctgattcgt ctttcacaag tgtcttcaga tgttgatgaa 120
251 caactgtcca agtcagttaa agataaggta ttgtgcctt gccgttacaa ctctccgcat 180
252 gaagatgagt ctgaagaccg aatctactgg caaaaacatg acaaagtggg gctgtctgtc 240
253 attgctggga aactaaaagt gtggcccgag tataagaacc ggactttata tgacaacact 300
254 acctactctc ttatcatcct gggcctggtc ctttcagacc ggggcacata cagctgtgtc 360
255 gttcaaaaaga aggaagaggg aacgtatgaa gttaaacact tggctttagt aaagtgtgcc 420
256 atcaagctg acttctctac ccccaacata actgagtcgt gaaacccatc tgcagacact 480
257 aaaaggatta cctgctttgc ttccgggggt ttccaaaagc ctgccttctc ttggttgtaa 540
258 aatggaagag aattacctgg catcaatacg acaatttccc aggatcctga atctgaattg 600
259 tacaccatta gtgcccaact agatttcaat acgactcgca accacacat taagtgtctc 660
260 attaaatatg gagatgctca cgtgtcagag gacttcacct gggaaaaacc cccagaagac 720
261 cctcctgata gcaagcccg ggggtgtggg agcgggtgtg gcggcagtg gcggcgcgga 780
262 actagtaata gtgactctga atgtcccctg tcccacgatg ggtactgct ccatgatggt 840
263 gtgtgcatgt atattgaagc attggacaag tatgcatgca actgtgtgtg tggctacatc 900
264 ggggagcgat gtcagtaccg agacctgaag tggtgggaac tgcgc 945

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266 <210> SEQ ID NO: 8
267 <211> LENGTH: 47
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
273 OLIGONUCLEOTIDE

```

VERIFICATION SUMMARY DATE: 05/18/2000
PATENT APPLICATION: US/09/445,375 TIME: 12:23:31

Input Set : A:\DU23SEQ.txt
Output Set: N:\CRF3\05182000\I445375.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:31 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:31 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:35 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:35 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:42 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:42 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:59 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:59 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:62 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:62 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:66 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:66 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:70 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:70 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:73 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:73 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:75 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:75 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:76 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:76 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:80 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:80 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:81 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:81 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:82 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:82 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:83 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:83 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:85 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:85 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:87 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:87 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:89 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:89 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:103 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:103 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3

VERIFICATION SUMMARY DATE: 05/18/2000
PATENT APPLICATION: US/09/445,375 TIME: 12:23:31

Input Set : A:\DU23SEQ.txt
Output Set: N:\CRF3\05182000\I445375.raw

L:103 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:105 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:105 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:107 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:108 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:108 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:112 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:112 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:143 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:474 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:477 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24